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1647

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/981,649A

DATE: 03/12/2002 ^{PS}
TIME: 10:06:37

Input Set : A:\37665seq.txt

Output Set : N:\CRF3\03122002\I981649A.raw

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 AUG 15 2002
 TECH CENTER 1600/2900

3 <110> APPLICANT: Ford et al.
 5 <120> TITLE OF INVENTION: EGF MOTIF PROTEIN, EGFL6, MATERIALS AND METHODS
 7 <130> FILE REFERENCE: 28110/37665
 9 <140> CURRENT APPLICATION NUMBER: US 09/981,649A
 10 <141> CURRENT FILING DATE: 2001-10-15
 12 <150> PRIOR APPLICATION NUMBER: US 09/687,860
 13 <151> PRIOR FILING DATE: 2000-10-13
 15 <150> PRIOR APPLICATION NUMBER: US 09/620,312
 16 <151> PRIOR FILING DATE: 2000-07-19
 18 <150> PRIOR APPLICATION NUMBER: US 09/363,316
 19 <151> PRIOR FILING DATE: 1999-07-28
 21 <160> NUMBER OF SEQ ID NOS: 32
 23 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 300
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Homo sapiens
 30 <220> FEATURE:
 31 <221> NAME/KEY: CDS
 32 <222> LOCATION: (1)...(300)
 34 <220> FEATURE:
 35 <221> NAME/KEY: misc_feature
 36 <222> LOCATION: (1)...(300)
 37 <223> OTHER INFORMATION: n = A,T,C or G
 39 <220> FEATURE:
 40 <221> NAME/KEY: misc_feature
 41 <222> LOCATION: (84)
 42 <223> OTHER INFORMATION: Xaa = Any Amino Acid
 44 <400> SEQUENCE: 1
 45 ggc tgg aga aga aac agc aag gga gtc tgt gaa gct aca tgc gaa cct 48
 46 Gly Trp Arg Arg Asn Ser Lys Gly Val Cys Glu Ala Thr Cys Glu Pro
 47 1 5 10 15
 49 gga tgt aag ttt ggt gag tgc gtg gga cca aac aaa tgc aga tgc ttt 96
 50 Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys Arg Cys Phe
 51 20 25 30
 55 cca gga tac acc ggg aaa acc tgc agt caa gat gtg aat gag tgt gga 144
 56 Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn Glu Cys Gly
 57 35 40 45
 59 atg aaa ccc cgg cca tgc caa cac aga tgt gtg aat aca cac gga agc 192
 60 Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr His Gly Ser
 61 50 55 60
 64 tac aag tgc ttt tgc ctc agt ggc cac atg ctc atg cca gat gct acg 240
 65 Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro Asp Ala Thr

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```

66      65      70      75      80
W--> 68  tgt gtg aac tcn agg aca tgt gcc atg ata aac tgt cag tat agc tgt      288
W--> 69  Cys Val Asn Xaa Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys
70      85      90      95
71  gaa gac aca gaa      300
72  Glu Asp Thr Glu
73      100
76 <210> SEQ ID NO: 2
77 <211> LENGTH: 1611
78 <212> TYPE: DNA
79 <213> ORGANISM: Homo sapiens
81 <220> FEATURE:
82 <221> NAME/KEY: CDS
83 <222> LOCATION: (1)...(1506)
85 <220> FEATURE:
86 <221> NAME/KEY: misc_feature
87 <222> LOCATION: (1)...(1611)
88 <223> OTHER INFORMATION: n = A,T,C or G
90 <220> FEATURE:
91 <221> NAME/KEY: misc_feature
92 <222> LOCATION: (84)
93 <223> OTHER INFORMATION: Xaa = Any Amino Acid
95 <220> FEATURE:
96 <221> NAME/KEY: misc_feature
97 <222> LOCATION: (501)
98 <223> OTHER INFORMATION: Xaa = Any Amino Acid
100 <220> FEATURE:
101 <221> NAME/KEY: misc_feature
102 <222> LOCATION: (502)
103 <223> OTHER INFORMATION: Xaa = Any Amino Acid
106 <400> SEQUENCE: 2
107  ggc tgg aga aga aac agc aag gga gtc tgt gaa gct aca tgc gaa cct      48
108  Gly Trp Arg Arg Asn Ser Lys Gly Val Cys Glu Ala Thr Cys Glu Pro
109  1      5      10      15
111  gga tgt aag ttt ggt gag tgc gtg gga cca aac aaa tgc aga tgc ttt      96
112  Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys Arg Cys Phe
113      20      25      30
115  cca gga tac acc ggg aaa acc tgc agt caa gat gtg aat gag tgt gga      144
116  Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn Glu Cys Gly
117      35      40      45
119  atg aaa ccc cgg cca tgc caa cac aga tgt gtg aat aca cac gga agc      192
120  Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr His Gly Ser
121      50      55      60
123  tac aag tgc ttt tgc ctc agt ggc cac atg ctc atg cca gat gct acg      240
124  Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro Asp Ala Thr
125  65      70      75      80
W--> 127  tgt gtg aac tcn agg aca tgt gcc atg ata aac tgt cag tat agc tgt      288
W--> 128  Cys Val Asn Xaa Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys
129      85      90      95

```

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Input Set : A:\37665seq.txt

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131	gaa gac aca gaa gaa ggg cca cag tgc ctg tgt cca tcc tca gga ctc	336
132	Glu Asp Thr Glu Glu Gly Pro Gln Cys Leu Cys Pro Ser Ser Gly Leu	
133	100 105 110	
135	cgc ctg gcc cca aat gga aga gac tgt cta gat att gat gaa tgt gcc	384
136	Arg Leu Ala Pro Asn Gly Arg Asp Cys Leu Asp Ile Asp Glu Cys Ala	
137	115 120 125	
139	tct ggt aaa gtc atc tgt ccc tac aat cga aga tgt gtg aac aca ttt	432
140	Ser Gly Lys Val Ile Cys Pro Tyr Asn Arg Arg Cys Val Asn Thr Phe	
141	130 135 140	
142	gga agc tac tac tgc aaa tgt cac att ggt ttc gaa ctg caa tat atc	480
143	Gly Ser Tyr Tyr Cys Lys Cys His Ile Gly Phe Glu Leu Gln Tyr Ile	
144	145 150 155 160	
147	agt gga cga tat gac tgt ata gat ata aat gaa tgt act atg gat agc	528
148	Ser Gly Arg Tyr Asp Cys Ile Asp Ile Asn Glu Cys Thr Met Asp Ser	
149	165 170 175	
152	cat acg tgc agc cac cat gcc aat tgc ttc aat acc caa ggg tcc ttc	576
153	His Thr Cys Ser His His Ala Asn Cys Phe Asn Thr Gln Gly Ser Phe	
154	180 185 190	
156	aag tgt aaa tgc aag cag gga tat aaa ggc aat gga ctt cgg tgt tct	624
157	Lys Cys Lys Cys Lys Gln Gly Tyr Lys Gly Asn Gly Leu Arg Cys Ser	
158	195 200 205	
160	gct atc cct gaa aat tct gtg aag gaa gtc ctc aga gca cct ggt acc	672
161	Ala Ile Pro Glu Asn Ser Val Lys Glu Val Leu Arg Ala Pro Gly Thr	
162	210 215 220	
164	atc aaa gac aga atc aag aag ttg ctt gct cac aaa aac agc atg aaa	720
165	Ile Lys Asp Arg Ile Lys Lys Leu Leu Ala His Lys Asn Ser Met Lys	
166	225 230 235 240	
168	aag aag gca aaa att aaa aat gtt acc cca gaa ccc acc agg act cct	768
169	Lys Lys Ala Lys Ile Lys Asn Val Thr Pro Glu Pro Thr Arg Thr Pro	
170	245 250 255	
172	acc cct aag gtg aac ttg cag ccc ttc aac tat gaa gag ata gtt tcc	816
173	Thr Pro Lys Val Asn Leu Gln Pro Phe Asn Tyr Glu Glu Ile Val Ser	
174	260 265 270	
176	aga ggc ggg aac tct cat gga ggt aaa aaa ggg aat gaa gag aaa atg	864
177	Arg Gly Gly Asn Ser His Gly Gly Lys Lys Gly Asn Glu Glu Lys Met	
178	275 280 285	
180	aaa gag ggg ctt gag gat gag aaa aga gaa gag aaa gcc ctg aag aat	912
181	Lys Glu Gly Leu Glu Asp Glu Lys Arg Glu Glu Lys Ala Leu Lys Asn	
182	290 295 300	
184	gac ata gag gag cga agc ctg cga gga gat gtg ttt ttc cct aag gtg	960
185	Asp Ile Glu Glu Arg Ser Leu Arg Gly Asp Val Phe Phe Pro Lys Val	
186	305 310 315 320	
190	aat gaa gca ggt gaa ttc ggc ctg att ctg gtc caa agg aaa gcg cta	1008
191	Asn Glu Ala Gly Phe Gly Leu Ile Leu Val Gln Arg Lys Ala Leu	
192	325 330 335	
194	act tcc aaa ctg gaa cat aaa gat tta aat atc tcg gtt gac tgc agc	1056
195	Thr Ser Lys Leu Glu His Lys Asp Leu Asn Ile Ser Val Asp Cys Ser	
196	340 345 350	
198	ttc aat cat ggg atc tgt gac tgg aaa cag gat aga gaa gat gat ttt	1104

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199 Phe Asn His Gly Ile Cys Asp Trp Lys Gln Asp Arg Glu Asp Asp Phe
200          355          360          365
201 gac tgg aat cct gct gat cga gat aat gct att ggc ttc tat atg gca      1152
202 Asp Trp Asn Pro Ala Asp Arg Asp Asn Ala Ile Gly Phe Tyr Met Ala
203          370          375          380
205 gtt ccg gcc ttg gca ggt cac atg aaa gac att ggc cga ttg aaa ctt      1200
206 Val Pro Ala Leu Ala Gly His Met Lys Asp Ile Gly Arg Leu Lys Leu
207          385          390          395          400
209 ctc cta cct gac ctg caa ccc caa agc aac ttc tgt ttg ctc ttt gat      1248
210 Leu Leu Pro Asp Leu Gln Pro Gln Ser Asn Phe Cys Leu Leu Phe Asp
211          405          410          415
213 tac cgg ctg gcc gga gac aaa gtc ggg aaa ctt cga gtg ttt gtg aaa      1296
214 Tyr Arg Leu Ala Gly Asp Lys Val Gly Lys Leu Arg Val Phe Val Lys
215          420          425          430
217 aac agt aac aat gcc ctg gca tgg gag aag acc acg agt gag gat gaa      1344
218 Asn Ser Asn Asn Ala Leu Ala Trp Glu Lys Thr Thr Ser Glu Asp Glu
219          435          440          445
221 aag tgg aag aca ggg aaa att cag ttg tat caa gga act gat gct acc      1392
222 Lys Trp Lys Thr Gly Lys Ile Gln Leu Tyr Gln Gly Thr Asp Ala Thr
223          450          455          460
225 aaa agc atc att ttt gaa gca gaa cgt ggc aag ggc aaa acc ggc gaa      1440
226 Lys Ser Ile Ile Phe Glu Ala Glu Arg Gly Lys Gly Lys Thr Gly Glu
227          465          470          475          480
229 atc gca gtg gat ggc gtc ttg ctt gtt tca ggc tta tgt cca gat agc      1488
230 Ile Ala Val Asp Gly Val Leu Leu Val Ser Gly Leu Cys Pro Asp Ser
231          485          490          495
W--> 233 ctt tta tct gtg gan nnc tgaatggtac tatctttata tttgactttg      1536
W--> 234 Leu Leu Ser Val Xaa Xaa
235          500
237 tatgtcagtt ccttggtttt ttgatattg catcatagga cctctggcat tttaaaatta      1596
238 ctactgaaa aattg      1611
240 <210> SEQ ID NO: 3
241 <211> LENGTH: 100
242 <212> TYPE: PRT
243 <213> ORGANISM: Homo sapiens
245 <400> SEQUENCE: 3
246 Gly Trp Arg Arg Asn Ser Lys Gly Val Cys Glu Ala Thr Cys Glu Pro
247 1          5          10          15
248 Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys Arg Cys Phe
249          20          25          30
250 Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn Glu Cys Gly
251          35          40          45
253 Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr His Gly Ser
254          50          55          60
255 Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro Asp Ala Thr
256          65          70          75          80
257 Cys Val Asn Ser Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys
258          85          90          95
259 Glu Asp Thr Glu

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
Input Set : A:\37665seq.txt

Output Set: N:\CRF3\03122002\I981649A.raw

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263 <211> LENGTH: 537
264 <212> TYPE: PRT
265 <213> ORGANISM: Homo sapiens
267 <220> FEATURE:
268 <221> NAME/KEY: misc_feature
269 <222> LOCATION: (503)
270 <223> OTHER INFORMATION: Xaa = Any Amino Acid
272 <400> SEQUENCE: 4
273 Gly Trp Arg Arg Asn Ser Lys Gly Val Cys Glu Ala Thr Cys Glu Pro
274   1          5          10          15
276 Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys Arg Cys Phe
277          20          25          30
278 Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn Glu Cys Gly
279          35          40          45
280 Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr His Gly Ser
281          50          55          60
282 Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro Asp Ala Thr
283          65          70          75          80
284 Cys Val Asn Ser Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys
285          85          90          95
286 Glu Asp Thr Glu Glu Gly Pro Gln Cys Leu Cys Pro Ser Ser Gly Leu
287          100         105         110
288 Arg Leu Ala Pro Asn Gly Arg Asp Cys Leu Asp Ile Asp Glu Cys Ala
289          115         120         125
290 Ser Gly Lys Val Ile Cys Pro Tyr Asn Arg Arg Cys Val Asn Thr Phe
291          130         135         140
292 Gly Ser Tyr Tyr Cys Lys Cys His Ile Gly Phe Glu Leu Gln Tyr Ile
293          145         150         155         160
294 Ser Gly Arg Tyr Asp Cys Ile Asp Ile Asn Glu Cys Thr Met Asp Ser
295          165         170         175
296 His Thr Cys Ser His His Ala Asn Cys Phe Asn Thr Gln Gly Ser Phe
297          180         185         190
298 Lys Cys Lys Cys Lys Gln Gly Tyr Lys Gly Asn Gly Leu Arg Cys Ser
299          195         200         205
300 Ala Ile Pro Glu Asn Ser Val Lys Glu Val Leu Arg Ala Pro Gly Thr
301          210         215         220
302 Ile Lys Asp Arg Ile Lys Lys Leu Leu Ala His Lys Asn Ser Met Lys
303          225         230         235         240
304 Lys Lys Ala Lys Ile Lys Asn Val Thr Pro Glu Pro Thr Arg Thr Pro
305          245         250         255
306 Thr Pro Lys Val Asn Leu Gln Pro Phe Asn Tyr Glu Glu Ile Val Ser
307          260         265         270
308 Arg Gly Gly Asn Ser His Gly Gly Lys Lys Gly Asn Glu Glu Lys Met
309          275         280         285
310 Lys Glu Gly Leu Glu Asp Glu Lys Arg Glu Glu Lys Ala Leu Lys Asn
311          290         295         300
312 Asp Ile Glu Glu Arg Ser Leu Arg Gly Asp Val Phe Phe Pro Lys Val

```


 Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

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L:68 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:69 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:127 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:128 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:233 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:234 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:336 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:455 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:509 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:574 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:663 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:665 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:667 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:752 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:754 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:756 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:836 M:283 W: Missing Blank Line separator, <220> field identifier
L:878 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:880 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:882 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:921 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1072 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:1457 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:1469 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1474 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1478 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1482 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1486 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1490 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1494 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1498 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1502 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1506 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1510 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1514 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1518 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1522 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1526 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1530 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1534 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1538 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1542 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1546 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1550 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1554 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1558 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1562 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1566 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27

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L:1570 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1574 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1578 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1582 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1586 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1590 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1594 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1598 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1602 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1606 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1755 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
L:1768 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:1772 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:1777 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:1781 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:1785 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:1789 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:1793 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:1797 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:1801 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:1805 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:1809 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:1813 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:1817 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:1821 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29